

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2000, 19:16:21 : Search time 727.75 Seconds

(without alignments)
2737.911 Million cell updates/sec

Title: US-09-227-881-2

Perfect score: 5304
Sequence: 1 acctgtgtcagtttaccctc.....cagcacccttcagcaccagc 5304

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_36: *
1: /cgn2_2/gcgdata/geneseq/geneseqn/NA1980.DAT: *
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5: /cgn2_2/gcgdata/geneseq/geneseqn/NA1984.DAT: *
6: /cgn2_2/gcgdata/geneseq/geneseqn/NA1985.DAT: *
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20: /cgn2_2/gcgdata/geneseq/geneseqn/NA1999.DAT: *
21: /cgn2_2/gcgdata/geneseq/geneseqn/NA2000.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5296	99.8	5304	19	V51364 Human TIGR promote
2	5279.6	99.5	5300	19	V51362 Human TIGR promote
3	5279.6	99.5	5300	19	V51363 Human TIGR promote
4	5279.6	99.5	5300	19	V51365 Human TIGR promote
5	5279.6	99.5	5300	19	V51366 Human TIGR promote
6	5279.6	99.5	5300	19	V51367 Human TIGR promote
7	5277	99.5	5299	19	V51361 Human TIGR promote
8	5253.4	99.0	6169	19	V51368 Human TIGR upstrea
9	1836	34.6	2800	21	Z37968 Human GLCIA gene e
C 10	176.4	3.3	283	15	A22 sequence dbcl.
C 11	175.2	3.3	162450	21	Retinoblastoma bin
C 12	174.2	3.3	282	18	T62346 Consensus Alu repe

C 13	173.6	3.3	17327	14	O44278
C 14	173.2	3.3	49999	20	Z23900
C 15	172.8	3.3	452	17	POLYMERLOC
C 16	172.8	3.3	106746	21	A10225
C 17	172	3.2	2932	13	O25388
C 18	172	3.2	2932	20	Z32161
C 19	172	3.2	2932	20	Z32162
C 20	172	3.2	43069	21	Z36335
C 21	171.6	3.2	10380	18	T67164
C 22	171.2	3.2	21721	20	X83427
C 23	171.2	3.2	22976	20	X83426
C 24	171	3.2	54548	21	Z45596
C 25	170.8	3.2	2617	21	A23452
C 26	170.4	3.2	3234	16	O92781
C 27	170	3.2	15056	19	V52967
C 28	170	3.2	15056	21	Z99933
C 29	169.6	3.2	2426	18	A06689
C 30	169	3.2	5543	18	T75284
C 31	168.4	3.2	11288	16	O90512
C 32	168.2	3.2	3089	21	Z64958
C 33	167.4	3.2	555	20	V90098
C 34	167.4	3.2	41783	21	A35099
C 35	167.4	3.2	138169	21	A34791
C 36	167.4	3.2	141589	21	A35005
C 37	167.4	3.2	141589	21	A35030
C 38	167.4	3.2	162450	21	Z86967
C 39	166.8	3.1	7849	16	O94109
C 40	166.4	3.1	1601	21	A35191
C 41	166.4	3.1	1601	21	Z46814
C 42	166.4	3.1	1618	12	O10207
C 43	166.4	3.1	1618	14	O46958
C 44	166.4	3.1	1618	21	Z86905
C 45	166.4	3.1	1645	21	Z58659

ALIGNMENTS

RESULT 1	
V51364	
ID V51364 standard; DNA: 5304 BP.	
XX V51364:	
AC	
XX	
DT 27-OCT-1998 (first entry)	
XX	
DE Human TIGR promoter mutant TIGRmt3 DNA.	
XX	
KW TIGR: trabecular meshwork induced glucocorticoid response protein; human;	
KW diagnosis; glaucoma; polymorphism; steroid sensitivity; mutant; ss.	
XX	
OS Homo sapiens.	
OS Synthetic.	
XX	
FH Key	Location/Qualifiers
FT mutation	4997..5002
FT	/*tag= a
ET	/note= "Wild-type TG is replaced with TGTGTC"
XX	
PN W09832850-A1.	
XX	
PD 30-JUL-1998.	
XX	
PE 09-JAN-1998; 98WO-US00468.	
XX	
PR 26-SEP-1997; 97US-0938669.	
XX	
PR 28-JAN-1997; 97US-0791154.	
XX	
PA (REGC) UNIV CALIFORNIA.	
XX	
PI Chen H, Chen P, Nguyen TD, Polansky JR;	
XX	
DR WPI: 1998-427946/36.	

Serglycin - proteo
Human LOBO homolog
POLYMERLOC
Human PCRA-1 genom
TXA2 receptor gene
Human thromboxane
Human endothelial
Genomic sequence o
Human alpha-N-acet
Human lipolysis st
Genomic region con
DNA sequence of th
cDNA encoding huma
Human thymopoietin
Cardiomyoblastic
DNA sequence of co
Human Immunogenic
Nucleotide sequenc
CEA clone HindIII-
Membrane-bound pro
EST clone CW1682.
Human adenosine re
Human adenosine re
Human adenosine re
Human adenosine re
Retinoblastoma bin
hML genomic DNA.
Human adenosine re
Interleukin-10 (IL
PHISc Insert conta
Human cytokine syn
Human CSF coding
Human Interleukin-

XX Use of TIGR nucleic acid sequences - used for, e.g. developing
PT products for diagnosis, prognosis and treatment of glaucoma
XX
XX Disclosure: Fig 2; 105bp; English.
XX
XX This sequence is a trabecular meshwork induced glucocorticoid response
CC protein (TIGR) promoter mutant, TIGRm3, which is used in a method for
CC diagnosing glaucoma in a patient. The method involves the detection of
CC polymorphisms whose presence is predictive of a mutation affecting TIGR
CC response in the patient and can be diagnostic of glaucoma or steroid
CC sensitivity. Base substitutions and base additions upstream of and within
CC TIGR exons can also be used to diagnose glaucoma.
XX
XX Sequence 5304 BP: 1482 A: 1152 C: 1237 G: 1433 T: 0 other:
SO
Query Match 99.8% Score 5296; DB 19; Length 5304;
Best Local Similarity 99.9% Pred. No. 0;
Matches 5299; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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DB 1 attcttggttaagttacctcagggtctatttgaaatgaaatgataaccatgtgaaag 60
OY 61 tctataaactgtatagccctccatcctcgatgtatgtcttggcaggatgataaagaatca 120
DB 61 tctataaactgtatagccctccatcctcgatgtatgtcttggcaggatgataaagaatca 120
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DB 181 caagatgtgtctcttgaaagaagctatctctcaggaaacacacatccaatgtgaatc 240
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DB 361 atgaaggaacaaatcaatgaaatgaaggaaacagctcagaaaaaagatgttccaaatgg 420
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 Oy 3961 aagaaatagaatctttagggcaaacgtgttcttccacactgtgaggtgaggtcgcagagc 4020
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Db 5281 catccagagcactctcagcacagc 5304

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RESULT 2
V51362
ID V51362 standard; DNA; 5300 BP.
AC V51362;
XX 27-OCT-1998 (first entry)
DT
XX
DE Human TIGR promoter mutant TIGRmt1 DNA.
XX
KW TIGR: trabecular meshwork induced glucocorticoid response protein; human;
KW diagnosis: glaucoma; polymorphism; steroid sensitivity; mutant; ss.
XX
OS Homo sapiens.
XX Synthetic.
FH Key Location/Qualifiers
FT mutation 4337
FT /tag= a
FT /note= "Wild type C is replaced by G"
XX
PN WO9832850-A1.
XX
XX 30-JUL-1998.
XX
XX 09-JAN-1998; 98MO-US00468.
XX
XX 26-SEP-1997; 97US-0938669.
XX 28-JUN-1997; 97US-0791154.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
PI Chen H, Chen P, Nguyen TD, Polansky JR:
XX
XX WPI: 1998-427946/36.
XX
XX Use of TIGR nucleic acid sequences - used for, e.g. developing
PT products for diagnosis, prognosis and treatment of glaucoma
XX
XX PS Disclosure: Fig 2: 105pp; English.
XX
XX This sequence is a trabecular meshwork induced glucocorticoid response
XX protein (TIGR) promoter mutant, TIGRmt1, which is used in a method for
XX diagnosing glaucoma in a patient. The method involves the detection of
XX polymorphisms whose presence is predictive of a mutation affecting TIGR
XX response in the patient and can be diagnostic of glaucoma or steroid
XX sensitivity. Base substitutions and base additions upstream of and within
XX TIGR exons can also be used to diagnose glaucoma.
XX
SQ Sequence 5300 BP; 1482 A; 1151 C; 1236 G; 1431 T; 0 other:

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Query Match 99.5%; Score 5279.6; DB 19; Length 5300;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 5296; Conservativity 0; Mismatches 4; Indels 4; Gaps 1;

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Oy 1 attctgttaagtttaacctagggcttatatgaatgaatgataacaaatgtgaag 60
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Db 1 attctgttaagtttaacctagggcttatatgaatgaatgataacaaatgtgaag 60

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Oy	61	tcataataactgtatagatgcccctccatcttgagatgtatgtatgtctcttgccagagatgataaagaatca	120
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Oy	121	ggaagaagagatgtccacgtttacgcgttaacagagctgcacagctgtgtctctcttattttaa	180
Db	121	ggaagaagagaggtatccacgtttacgcgtttacagagctgcacagctgtgtctctcttattttaa	180
Oy	181	cagaatgtgtctcttgacacagagacttatctcttcaggaatacacaatcacaataatgtttaaact	240
Db	181	cagaatgtgtctcttgacacagagacttatctcttcaggaatacacaatcacaataatgtttaaact	240
Oy	241	catcaataacagagagacttaagaataacagaaatgaatgtgacctgtgtcccaagagaataatgcag	300
Db	241	catcaataacagagagacttaagaataacagaaatgaatgtgacctgtgtcccaagagaataatgcag	300
Oy	301	gagagacaaataatgatagaataaataaactcttccctgtgttttaatttcagagaataaagt	360
Db	301	gagagacaaataatgatagaataaataaactcttccctgtgttttaatttcagagaataaagt	360
Oy	361	atgagagccaaaatacaatgaataagaaataaagctccagataaataaagaatgtttcccaatg	420
Db	361	atgagagccaaaatacaatgaataagaaataaagctccagataaataaagaatgtttcccaatg	420
Oy	421	taattaaagtattgttctctcttgaggagaagacctccatgtgagctgtatgtgagaataatggaa	480
Db	421	taattaaagtattgttctctcttgaggagaagacctccatgtgagctgtatgtgagaataatggaa	480
Oy	481	aaacagtcataaagaacgtgtatctcgatccagaatcccaagaggtatatttttaaaaccagat	540
Db	481	aaacagtcataaagaacgtgtatctcgatccagaatcccaagaggtatatttttaaaaccagat	540
Oy	541	ggacatcacctctgvggagcagaatctcagagaaggttcatgtttaagcaaaagacatacaataaac	600
Db	541	ggacatcacctctgvggagcagaatctcagagaaggttcatgtttaagcaaaagacatacaataaac	600
Oy	601	agcaaaaatcaaaaattccggcaaatgcagagaaatvggagacttggagaaacttccataac	660
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Oy	661	agtgatataggcagtttgacatgtttgcacaacatcccccgtctatccagggagaacaataa	720
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Oy	721	atctaacgggcttaagcccttgagacttccaaagagaataatgaaataactgcagagcaaaacaaa	780
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Db	781	gacatggttlaaaagagcaaaccaagaacatatgtgagaccttcaaaagcagatgtccctcagca	840
Oy	841	gggagccctgagagcaattgtgacctttaagaagaagccagtttcttaaggaatacttaagaatact	900
Db	841	gggagccctgagagcaattgtgacctttaagaagaagccagtttcttaaggaatacttaagaatact	900
Oy	901	ctgaaagatcatgaaattttaaccattttaagatctaaacaaataatgcagatgcaataacag	960
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Db	961	cttaagaatagggtcccaattttaaaagtcagagcatacaagaataacgtgtccagctcc	1020
Oy	1021	ggataaggttcgaaatactatttgaaatacaacgtgtgtcccaatccataattttcaagaatgac	1080
Db	1021	ggataaggttcgaaatactatttgaaatacaacgtgtgtcccaatccataattttcaagaatgac	1080
Oy	1081	tgtcatatgccccttcacacagagcccgatgtgtcttgagccttaacaaacacatctcaaaccca	1140
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Db	1141	gtgcctcaaccattgttaacgtgtcaatcttcagtgtagtccattacaattgcacctcccc	1200
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Oy	1261	tacagccagaagctccgtgtgaagggtgaagggtctgtctcttaacacttaactgtatctaac	1320
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Oy	1441	gtttcaccaatctagcccgctgtgtctgtgaactctctgaactccctgaagtgtatccacccctc	1500
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Oy	1501	agccctccctaagtgctgtggattacacgcatatgataccgcgcgccgccaagggtcagtgct	1560
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Dp	3541	gtctctagagagcagggcctatatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	3600
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Db 5277 catcagagcactctcagcagcagc 5300

RESULT 4
ID V51365 standard; DNA; 5300 BP.
XX
AC V51365:
XX
DT 27-OCT-1998 (first entry)
DE Human TIGR promoter mutant TIGRm14 DNA.
KM TIGR: trabecular meshwork induced glucocorticoid response protein; human;
KW diagnosis: glaucoma; polymorphism; steroid sensitivity; mutant; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT mutation 4256
FT /*tag= a
FT /note= "Wild-type A is replaced by G"
XX
PN M09832850-A1.
XX
PD 30-JUL-1998.
XX
PF 09-JAN-1998; 98MO-US00468.
XX
PR 26-SEP-1997; 97US-0938669.
XX
PR 28-JAN-1997; 97US-0791154.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Chen H, Chen P, Nguyen TD, Polansky JR;
XX
DR WPI: 1998-427946/36.
XX
PT Use of TIGR nucleic acid sequences - used for, e.g. developing
```

```
PT products for diagnosis, prognosis and treatment of glaucoma
XX
XX Disclosure: Fig 2; 105bp; English.
XX
CC This sequence is a trabecular meshwork induced glucocorticoid response
CC protein (TIGR) promoter mutant, TIGRm14, which is used in a method for
CC diagnosing glaucoma in a patient. The method involves the detection of
CC polymorphisms whose presence is predictive of a mutation affecting TIGR
CC response in the patient and can be diagnostic of glaucoma or steroid
CC sensitivity. Base substitutions and base additions upstream of and within
CC TIGR exons can also be used to diagnose glaucoma.
XX
SQ Sequence 5300 BP; 1481 A; 1152 C; 1236 G; 1431 T; 0 other:

Query Match 99.5%; Score 5279.6; DB 19; Length 5300;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 5296; Conservative 0; Mismatches 4; Indels 4; Gaps 1;

Oy 1 atcttctcagtttaactcaggtctatctgaatgaatgaataaccatgtgaaag 60
Db 1 atcttctcagtttaactcaggtctatctgaatgaatgaataaccatgtgaaag 60
Oy 61 tccataaactgtataagcctccatctggatgtatgtcttgcagagatgaataatca 120
Db 61 tccataaactgtataagcctccatctggatgtatgtcttgcagagatgaataatca 120
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Oy 181 cagatgtgtcctcgtacagaagctatctctcagaagaacatcacatcaatatgttaatc 240
Db 181 cagatgtgtcctcgtacagaagctatctctcagaagaacatcacatcaatatgttaatc 240
Oy 241 catcaaacagagcttaagaaacaggaatgagatggtgaccttgcctcaagaaatgccaag 300
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Oy 301 gagaagcaaatgaatgaataataataaactttcccttgttttaatttcaggaaataatg 360
Db 301 gagaagcaaatgaatgaataataataaactttcccttgttttaatttcaggaaataatg 360
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Dh 841 gggagccctgagcattgtgctttagaaggccagtttcttaaggatcttaagaacc 900
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QY	3241	tccttaagcataagacaatctgcatcttgcataataccaaaagaaatgcagagactaaactgtct	33000
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QY	3361	ttaaacttttaaccttgacacagaccacccacgcagctcagcagctgagctgcagacagcg	34200

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Db 3421 agtgcaccgcgcagcagggagagaaagaaagagagagatgagtgatgagacaagaag 3480
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Oy 5281 catcagagacacctcagacagc 5304
Db 5277 catcagagacacctcagacagc 5300

RESULT 6
V51367
ID V51367 standard; DNA: 5300 BP.
XX
AC V51367:
XX
DT 27-OCT-1998 (first entry)
XX
DE Human TIGR promoter variant TIGRsv1 DNA.
XX
KW TIGR: trabecular meshwork induced glucocorticoid response protein; human;
KM diagnosis; glaucoma; polymorphism; steroid sensitivity; mutant; ss.
XX
OS Homo sapiens.

OS Synthetic.
XX Key Location/Qualifiers
FH 4406
FT mutation /tag- a
FT /note- "Wild-type A is replaced by G"
XX
XX MO9832850-A1.
XX
XX 30-JUL-1998.
XX
XX 09-JAN-1998; 98WO-US00468.
XX
XX 26-SEP-1997; 97US-0938669.
XX 28-JAN-1997; 97US-0791154.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Chen H, Chen P, Nguyen TD, Polansky JR;
XX
XX WPI: 1998-427946/36.
XX
XX use of TIGR nucleic acid sequences - used for, e.g. developing
XX products for diagnosis, prognosis and treatment of glaucoma
XX
XX Disclosure: Fig 2; 105pp; English.
XX
XX This sequence is a trabecular meshwork induced glucocorticoid response
XX protein (TIGR) promoter variant, TIGRsv1, which is used in a method for
XX diagnosing glaucoma in a patient. The method involves the detection of
XX polymorphisms whose presence is predictive of a mutation affecting TIGR
XX response in the patient and can be diagnostic of glaucoma or steroid
XX sensitivity. Base substitutions and base additions upstream of and within
XX TIGR exons can also be used to diagnose glaucoma.
XX
XX Sequence 5300 BP: 1481 A; 1152 C; 1236 G; 1431 T; 0 other;
SQ

Query Match 99.5% Score 5279.6; DB 19; Length 5300;
Best Local Similarity 99.8% Pred. No. 0;
Matches 5299; Conservative 0; Mismatches 4; Indels 4; Gaps 1;

QY 1 attcttctcaggttaccctcagggtatattgaaatgaaatgagataaccagtgaag 60
DB 1 attcttctcaggttaccctcagggtatattgaaatgaaatgagataaccagtgaag 60
QY 61 tccataaacgttatacctccatctcgatgatagtctcttgccagatgataaagaatca 120
DB 61 tccataaacgttatacctccatctcgatgatagtctcttgccagatgataaagaatca 120
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Oy	1621	taatttcagaagatctctctgggaatggggaatacgggccaatagagctgcctgtactgtccagac	1680
Dp	1621	taatttcagaagatctctctgggaatggggaatacgggccaatagagctgcctgtactgtccagac	1680
Oy	1681	cactgtgctccatcacactctctctcccaaccctcatcttcacagagctaaagttaacatttat	1740
Dp	1681	cactgtgctccatcacactctctctcccaaccctcatcttcacagagctaaagttaacatttat	1740
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Dp	1741	caaccatctcttctgtgtaaagcctcccaatcgttactgaataaagaagctataataactag	1800
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Dp	1801	tctcaattctgggggcacactgtgtgtgtataaagggaaggaagacataaccccgagaaccc	1860
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Dp	1921	tgggtgtctccagagcaaacctctgcagagcccggtgcacatggtgtgtttgtatacctctcag	1980
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Dp	2581	gctcaccagaatctcagtgctgtctcaacggggcctggagaggttctcagctctcctccgtgagc	2640
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Db	2701	ataaaagctcagctcgtttaaaataatccaaagcgtgtcgaatggtttctctcaacgaaagcccttat	2760
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Db	2881	tgcgaagacggttcgaaataacctctgaaatccagggagacccgaattctctctcgtgtctgacctat	2940
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Oy	3181	cagggcccgaaagggcccaaatgtcctctcggaaagctcgaatgaaccacaaacagccaaatttctct	3240
Db	3181	cagggcccgaaagggcccaaatgtcctctcggaaagctcgaatgaaccacaaacagccaaatttctct	3240
Oy	3241	tcccccagaacataagacaatctgtgcattctggccaatacacaagaaagaaatgctcagaagactaaactgt	3300
Db	3241	tcccccagaacataagacaatctgtgcattctggccaatacacaagaaagaaatgctcagaagactaaactgt	3300
Oy	3301	ggtaagcctcttcgctgcattccaaaacactgggacagagcagatgtgaaatctccagagatctg	3360
Db	3301	ggtaagcctcttcgctgcattccaaaacactgggacagagcagatgtgaaatctccagagatctg	3360
Oy	3361	ttaaactcttcaacccctctgaccggcaaccccaacgagctcctcagctgtcgtcgaacaaacgg	3420
Db	3361	ttaaactcttcaacccctctgaccggcaaccccaacgagctcctcagctgtcgtcgaacaaacgg	3420
Oy	3421	agtgcacctgcgaacgagggagggagaaagaaagaaagagagatgatactgaaacaaagaaag	3480
Db	3421	agtgcacctgcgaacgagggagggagaaagaaagaaagagagatgatactgaaacaaagaaag	3480
Oy	3481	acagaatcattcaacaaagggcagttggtgaattgtgacacaaagggatttaagttccacgtgtactctgg	3540
Db	3481	acagaatcattcaacaaagggcagttggtgaattgtgacacaaagggatttaagttccacgtgtactctgg	3540
Oy	3541	gtcttcaggaagggcagggcctatatctgtgggggggggaaataatccagtctcaaggaagatctggggga	3600
Db	3541	gtcttcaggaagggcagggcctatatctgtgggggggggaaataatccagtctcaaggaagatctggggga	3600
Oy	3601	cttgatcttcaataatataatttctcccttaacaaagctggaaatctctcggcgaagctcaacag	3660
Db	3601	cttgatcttcaataatataatttctcccttaacaaagctggaaatctctcggcgaagctcaacag	3660
Oy	3661	gtatgaactggaagcgtgtgaagatctacttagttctccttatitgaagaaaccttttctctgt	3720
Db	3661	gtatgaactggaagcgtgtgaagatctacttagttctccttatitgaagaaaccttttctctgt	3720
Oy	3721	ggagcttgaagcagcaaaagggcaattcccggttctctttaaacagggaaagaaacattccctaaag	3780
Db	3721	ggagcttgaagcagcaaaagggcaattcccggttctctttaaacagggaaagaaacattccctaaag	3780

Dh	3721	ggagtttagcagcacaaaggcaatcccgcttctctttaacaggaagaaaacattcttaag	3780
Oy	3781	taagagccaaagagcttcaagcccttaggtctctgctgacataatgattggtttttgaaaat	3840
Dh	3781	taagagccaaagagcttcaagcccttaggtctctgctgacataatgattggtttttgaaaat	3840
Oy	3841	cattccagcgatggtttacatctcgatccgaaaaatgagctgtaccccttggccaagt	3900
Dh	3841	cattccagcgatggtttacatctcgatccgaaaaatgagctgtaccccttggccaagt	3900
Oy	3901	taaacaaacaccccatcttgtaaatgtcccaaggtccaggtctaacctcagaaacccaat	3960
Dh	3901	taaacaaacaccccatcttgtaaatgtcccaaggtccaggtctaacctcagaaacccaat	3960
Oy	3961	aagaatagaatctttaagagcaacctggtttctccactctggaggtagtctgcagggc	4020
Dh	3961	aagaatagaatctttaagagcaacctggtttctccactctggaggtagtctgcagggc	4020
Oy	4021	agcttgggaatatcttacttccaagatagacactgtgttggtattaaacataaagt	4080
Dh	4021	agcttgggaatatcttacttccaagatagacactgtgttggtattaaacataaagt	4080
Oy	4081	tgcccaaaaggcaacatattctcaagtggtcttaagtctctctgacagttttgttat	4140
Dh	4081	tgcccaaaaggcaacatattctcaagtggtcttaagtctctctgacagttttgttat	4140
Oy	4141	ttaattgacatctgcacatttgctctttgtttctctcttgggtttataatgtaaagcag	4200
Dh	4141	ttaattgacatctgcacatttgctctttgtttctctcttgggtttataatgtaaagcag	4200
Oy	4201	ggattatataacctcagttccaagaagccgtgtgaattgtgaagagaaaaataaagttt	4260
Dh	4201	ggattatataacctcagttccaagaagccgtgtgaattgtgaagagaaaaataaattt	4260
Oy	4261	tatttttaacccctctcaacaaatttaaacattttacattgctgcgaatagaagccataa	4320
Dh	4261	tgtttttacccctctcaactaaatttaaacattttccattgctgcgaatagaagccataa	4320
Oy	4321	ctcaaaagtgtgaaataagatgacctgtgatttttgcatcaataagaataccagacatt	4380
Dh	4321	ctcaaaagtgtgaaataagatgacctgtgatttttgcatcaataagaataccagacatt	4380
Oy	4381	ttataactatatataagttgtgtgcaggtagctgtgtgaagtgaataattatatacccaacta	4440
Dh	4381	ttataactatatataagttgtgtgcaggtagctgtgtgaagtgaataattatatacccaacta	4440
Oy	4441	cttggaaaattgagccctccctcgagacctgttttttaaacatataaataaacgttttaa	4500
Dh	4441	cttggaaaattgagccctccctcgagacctgttttttaaacatataaataaacgttttaa	4500
Oy	4501	attcttgatatcttgtaataacataatltcatatcatattgtttcccttgtaataattt	4560
Dh	4501	attcttgatatcttgtaataacataatltcatatcatattgtttcccttgtaataattt	4560
Oy	4561	atacatcttgaaacaacattctctcgagaagatccccaagattccacaatgagattcttgg	4620
Dh	4561	atacatcttgaaacaacattctctcgagaagatccccaagattccacaatgagattcttgg	4620
Oy	4621	catgcaacacacagagtaagaagactgtattagaagggttaacatgtgacattgtgtgccttga	4680
Dh	4621	catgcaacacacagagtaagaagactgtattagaagggttaacatgtgacattgtgtgccttga	4680
Oy	4681	tgcaagaacttgaaatacaagaagctctccccaagaatacagactgttttaaaagcttaagggt	4740
Dh	4681	tgcaagaacttgaaatacaagaagctctccccaagaatacagactgttttaaaagcttaagggt	4740
Oy	4741	aggggggaaaaatctgcctctctataagaaatgctctccctggagccgtgtgaagggtctc	4800
Dh	4741	aggggggaaaaatctgcctctctataagaaatgctctccctggagccgtgtgaagggtctc	4800
Oy	4801	ctctgtctctcgccgctgttatattttctctgtccctgctaagctttaaagactgttct	4860
Dh	4801	ctctgtctctcgccgctgttatattttctctgtccctgctaagctttaaagactgttct	4860

[illegible]

This sequence is a trabecular meshwork induced glucocorticoid response protein (TIGR) promoter region which is used in a method for diagnosing glaucoma in a patient. The method involves the detection of polymorphisms whose presence is predictive of a mutation affecting TIGR response in the

Oy	2041	fatvgabactabactvgcacacccagagacaaatvgvgacaagcagtcacg	2100
Db	2041	tattvgagactatatactgcacagacccagagcaaaatvgvgacaagcagtcacg	2100
Oy	2101	ccctaccctcgvgvgvgvggacagcttcttcattvggaagcgvgccgaagaataataagcca	2160
Db	2101	ccctaccctcgvgvgvgvggacagcttcttcattvggaagcgvgccgaagaataataagcca	2160
Oy	2161	gccaacttaaaccccgatgctcggaagaagaagaataaacaacactctctggaagaattvgg	2230
Db	2161	gccaacttaaaccccgatgctcggaagaagaagaataaacaacactctctggaagaattvgg	2220
Oy	2221	agcaacccttaacaaagccacactccctcctbaggcccccctgctccatcagtgcccgagag	2280
Db	2221	agcaacccttaacaaagccacactccctcctbaggcccccctgctccatcagtgcccgagag	2280
Oy	2281	cccccaagcccgagctctctccaagcctccctctctcaatcacagcgctcgcagctcgccct	2340
Db	2281	cccccaagcccgagctctctccaagcctccctctctcaatcacagcgctcgcagctcgccct	2340
Oy	2341	gcccgcgctcccgvgaaatcgctccctcggtcacatcgagctcvgaaagccctcgtgctccagct	2400
Db	2341	gcccgcgctcccgvgaaatcgctccctcggtcacatcgagctcvgaaagccctcgtgctccagct	2400
Oy	2401	ccagaaagggaaaatvgagagvggaaactagtcctaaacggagaaactcvgagvggagacgtgttc	2460
Db	2401	ccagaaagggaaaatvgagagvggaaactagtcctaaacggagaaactcvgagvggagacgtgttc	2460
Oy	2461	ctcacgagvggaaaagvggctctccacgctccagagaaattcccgvgvgvggagactcgcagvgag	2520
Db	2461	ctcacgagvggaaaagvggctctccacgctccagagaaattcccgvgvgvggagactcgcagvgag	2520
Oy	2521	ctgcagagvggaaaagvggctccacgctccagagaaattcccgvgvgvggagactcgcagvgag	2580
Db	2521	ctgcagagvggaaaagvggctccacgctccagagaaattcccgvgvgvggagactcgcagvgag	2580
Oy	2581	gctgcgcccagabgtcacagtgtgtgtctcacacggvgctcvggaagcttccgctgctccctgtgagc	2640
Db	2581	gctgcgcccagabgtcacagtgtgtgtctcacacggvgctcvggaagcttccgctgctccctgtgagc	2640
Oy	2641	ctttttatctctctcctcgtctctgtagagagaagaagcttatcttaatgaaagvgatgcagcttc	2700
Db	2641	ctttttatctctctcctcgtctctgtagagagaagaagcttatcttaatgaaagvgatgcagcttc	2700
Oy	2701	ataaagcgacgctgtgtaaaatctccagagctvggcacatggtttctccacgaagggcccttat	2760
Db	2701	ataaagcgacgctgtgtaaaatctccagagctvggcacatggtttctccacgaagggcccttat	2760
Oy	2761	ctaaatvggaaatataatvggaagagagacacatctccctbaggcgcttaatcacggaaagvgac	2820
Db	2761	ctaaatvggaaatataatvggaagagagacacatctccctbaggcgcttaatcacggaaagvgac	2820
Oy	2821	tgvgagctttctctctcatgtgtctctcctcvggcaactacacagccctcgtggtvggactvggcta	2880
Db	2821	tgvgagctttctctctcatgtgtctctcctcvggcaactacacagccctcgtggtvggactvggcta	2880
Oy	2881	ctgcaagagcggtcggaaaaccccttggaatccagagagacctcgtgttctcttcggtctcgccact	2940
Db	2881	ctgcaagagcggtcggaaaaccccttggaatccagagagacctcgtgttctcttcggtctcgccact	2940
Oy	2941	ggtctgagctvgcgagacgctvgggacagatgctctcctccctcvggcaatagctctctctgct	3000
Db	2941	ggtctgagctvgcgagacgctvgggacagatgctctcctccctccctcvggcaatagctctctctgct	3000
Oy	3001	ataaagacccctcgcagctctcgtgtctctcgttgaacacactccctcgtgtatctctctcgtgaggg	3060
Db	3001	ataaagacccctcgcagctctcgtgtctctcgttgaacacactccctcgtgtatctctcgtgaggg	3060
Oy	3061	ggatgcttggaaagvggaaagvggagcagagcctcggagacagctcgaacaaagvggagvggaggg	3120
Db	3061	ggatgcttggaaagvggaaagvggagcagagcctcggagacagctcgaacaaagvggagvggaggg	3120

[illegible]

[illegible]

Db	5277	caccagcgaacctctcagcacag	5299
RESULT	8		
ID	V51368	standard; DNA: 6169 BP.	
XX	XX		
AC	V51368:		
XX	XX		
DT	27-OCT-1998	(first entry)	
XX	XX		
DE	Human TIGR upstream region and exon 1 DNA.		
XX	XX		
KM	TIGR: trabecular meshwork induced glucocorticoid response protein: human:		
XX	diagnosis: glaucoma; polymorphism; steroid sensitivity; ss.		
OS	Homo sapiens.		
XX	XX		
FH	Key	Location/Qualifiers	
FT	exon	5301..5940	
FT		/tag= a	
FT		/number= 1	
FT	CDS	5337..6169	
FT		/tag= b	
FT		/product= "TIGR"	
FT	Intron	/note= "partial coding sequence"	
FT		5941..6169	
FT		/tag= c	
FT		/number= 1	
FT		/note= "partial intron sequence"	
XX	XX		
PN	W09832850-A1.		
XX	XX		
PD	30-JUL-1998.		
XX	XX		
PE	09-JAN-1998;	98WO-US00468.	
XX	XX		
PR	26-SEP-1997;	97US-0938669.	
PR	28-JAN-1997;	97US-0791154.	
XX	XX		
PA	(REGC) UNIV CALIFORNIA.		
XX	XX		
P1	Chen H, Chen P, Nguyen TD, Polansky JR;		
XX	XX		
DR	WPI: 1998-427946/36.		
XX	XX		
PT	Use of TIGR nucleic acid sequences - used for, e.g. developing		
XX	products for diagnosis, prognosis and treatment of glaucoma		
XX	XX		
P5	Claim 37; Fig 3; 105bp; English.		
XX	XX		
CC	This sequence is a trabecular meshwork induced glucocorticoid response		
CC	protein (TIGR) upstream region and exon 1. This DNA sequence can be used		
CC	in a method for diagnosing glaucoma in a patient. The method involves the		
CC	detection of polymorphisms whose presence is predictive of a mutation		
CC	affecting TIGR response in the patient and can be diagnostic of glaucoma		
CC	or steroid sensitivity. Base substitutions and base additions upstream of		
CC	and within TIGR exons can also be used to diagnose glaucoma.		
XX	XX		
SQ	Sequence 6169 BP; 1702 A; 1389 C; 1491 G; 1587 T; 0 other:		
Query Match	99.0%;	Score 5253.4;	DB 19; Length 6169;
Best Local Similarity	99.8%;	Pred. No. 0;	
Matches 52593;	Conservative 0;	Mismatches 6;	Indels 6; Gaps 3
OY	1	abctttgttcagtttactccacgagcgcatatagaatagaatgataccaatgtgaag	60
DB	1	atcttgctcagtttacccacgagcgcatattagaatgaatgatataccaatgtgaag	60
OY	61	tccctaacaactgtatagctccatccgcgatgtcatgtccttggcaggatataaagaatca	120
DB	61	tccctaacaactgtatagctccatccgcgatgtcatgtccttggcaggatataaagaatca	120

Oy	121	ggagagagagatataccacgcttaagccagctgtccaggctgtctgctgtctatttaagga	180
Db	121	ggaaagaaagaaatataccacgcttaagccagctgtccaggctgtctgctgtctatttaagga	180
Oy	181	cagatgtgtgctcccgacacagagcattctcttcagagaaactcaatccaaatcgtgaatc	240
Db	181	cagatgtgtgctcccgacacagagcattctcttcagagaaactcaatccaaatcgtgaatc	240
Oy	241	catccaacagagagcttaagaaacagaaatgaatgtgagcacttgcccaagggaaaaatgycag	300
Db	241	catccaacagagagcttaagaaacagaaatgaatgtgagcacttgcccaagggaaaaatgycag	300
Oy	301	gagagccaaatatagtatgaaaaataaactttccctttgtttttaattcagggaaaaatg	360
Db	301	gagagccaaatatagtatgaaaaataaactttccctttgtttttaattcagggaaaaatg	360
Oy	361	atgagagccaaatatagtatgaaaaataaactttccctttgtttttaattcagggaaaaatg	420
Db	361	atgagagccaaatatagtatgaaaaataaactttccctttgtttttaattcagggaaaaatg	420
Oy	421	taatbaagtatctgtctccttgagaaagacctccatcgtgagcttgaatgggaaaaatg	480
Db	421	taatbaagtatctgtctccttgagaaagacctccatcgtgagcttgaatgggaaaaatg	480
Oy	481	aaacgtccaagaagcttgatctgatacagctcccaagtgagattattttaaaaccagat	540
Db	481	aaacgtccaagaagcttgatctgatacagctcccaagtgagattattttaaaaccagat	540
Oy	541	ggcatcacctcgggagagacagatctcaagaagctcatgcttaagcaaaagacataacataac	600
Db	541	ggcatcacctcgggagagacagatctcaagaagctcatgcttaagcaaaagacataacataac	600
Oy	601	agcaaaatcaaaatctccgcgaatgagagaaatgaggactgggaaagcttcataac	660
Db	601	agcaaaatcaaaatctccgcgaatgagagaaatgaggactgggaaagcttcataac	660
Oy	661	agtgatgtgagagcttgagccatgtctcgaaacaactcccgctctatcacagggaaacaaa	720
Db	661	agtgatgtgagagcttgagccatgtctcgaaacaactcccgctctatcacagggaaacaaa	720
Oy	721	atcgatcgagcttaagccttgagacttccaaaggaaatatgaaaaactgagagcaaaacaaa	780
Db	721	atcgatcgagcttaagccttgagacttccaaaggaaatatgaaaaactgagagcaaaacaaa	780
Oy	781	gacatggttaaaagagcaaccagaaacatgtgagccttcaaaagcagatgccccacaga	840
Db	781	gacatggttaaaagagcaaccagaaacatgtgagccttcaaaagcagatgccccacaga	840
Oy	841	ggagaccggagagcattgagccttaagagagccaggtttcttaagagatcttaagaactc	900
Db	841	ggagaccggagagcattgagccttaagagagccaggtttcttaagagatcttaagaactc	900
Oy	901	ctgaagaatctcgtgaattttaaccattttaagataaaacaataatgcgaatgataatcag	960
Db	901	ctgaagaatctcgtgaattttaaccattttaagataaaacaataatgcgaatgataatcag	960
Oy	961	cttaagacatggtgtcccaattttaaaagtacagcatacaagataagtaagctgtccagctcc	1020
Db	961	cttaagacatggtgtcccaattttaaaagtacagcatacaagataagtaagctgtccagctcc	1020
Oy	1021	ggatcagagcagaataatcttaagaaatcacctgtgccccatcccaacttttcagaatgctc	1080
Db	1021	ggatcagagcagaataatcttaagaaatcacctgtgccccatcccaacttttcagaatgctc	1080
Oy	1081	tgctatagcccttcacacagagcccgatgtgctctgagccttaacacacatctcaacccaa	1140
Db	1081	tgctatagcccttcacacagagcccgatgtgctctgagccttaacacacatctcaacccaa	1140
Oy	1141	gtgcctcaaacatgtttaacggtgcatctcagttaagctcccatbaacaatgycacctccc	1200
Db	1141	gtgcctcaaacatgtttaacggtgcatctcagttaagctcccatbaacaatgycacctccc	1200

[illegible]

Dh	2281	cccccaagcccgagctcttccaaagcctccctcccaacagatcaagctgctcagcttcgcttc	2340
Oy	2341	gcccgcgtcccgctgaaatcgctccctggttgatctcgagctcgaaacctcttgctccaaagt	2400
Dh	2341	gcccgcgtcccggtgaaatcgctccctggttgatctcgagctcgaaacctcttgctccaaagt	2400
Oy	2401	ccagaaagaaatcgaaagggaaatactagctctaaacggaatactcgaaagggaagtgcttc	2460
Dh	2401	ccagaaagaaatcgaaagggaaatactagctctaaacggaatactcgaaagggaagtgcttc	2460
Oy	2461	ctcagaaagaaaggggagctcccaagctccaaaggaatactccaggggtcgagagctcgaaaggag	2520
Dh	2461	ctcagaaagaaaggggagctcccaagctccaaaggaatactccaggggtcgagagctcgaaaggag	2520
Oy	2521	tcgggaagcctcgagggctcgaaagggttgctctgaaagacagaaaggcgaaaggcgcaagctgaa	2580
Dh	2521	tcgggaagcctcgaggggtcgaaagggttgctctgaaagacagaaaggcgaaaggcgcaagctgaa	2580
Oy	2581	gcgcgccagatgctcagtgctgtgtctcaaggggctcgaaagtcttcgctgcttcctcgagc	2640
Dh	2581	gcgcgccagatgctcagtgctgtgtctcaaggggctcgaaagtcttcgctgcttcctcgagc	2640
Oy	2641	ctttcttcttctctcgtctcgcttggaagaaagaagcttatctcagaaaggatgcagtttc	2700
Dh	2641	ctttcttcttctctcgtctcgcttggaagaaagaagcttatctcagaaaggatgcagtttc	2700
Oy	2701	ataaagcgcagcctgtctaaanaattccaaagggtctcgacatgggtttctctccagaaaggccttat	2760
Dh	2701	ataaagcgcagcctgtctaaanaattccaaagggtctcgacatgggtttctctccagaaaggccttat	2760
Oy	2761	ttaa tcgggaatatagaaagacgagctcatcttctcagaagcgttlaattcacagaaagagtgagc	2820
Dh	2761	ttaa tcgggaatatagaaagacgagctcatcttctcagaagcgttlaattcacagaaagagtgagc	2820
Oy	2821	tcgaagctcttctctcaatgctctctcgggcaactaactaagccctgtgtgagctgtgacta	2880
Dh	2821	tcgaagctcttctctcaatgctctctcgggcaactaactaagccctgtgtgagctgtgacta	2880
Oy	2881	tcgaagaagcgggtcgaaanaacctctggaatacagaagagctcggtttctcttcggttcgcgcaat	2940
Dh	2881	tcgaagaagcgggtcgaaanaacctctggaatacagaagagctcggtttctcttcggttcgcgcaat	2940
Oy	2941	ggttcggtctgtcgagccga tcgggcaagctgctctctccctcccttcgggcaataagctctctgact	3000
Dh	2941	ggttcggtctgtcgagccga tcgggcaagctgctctctccctcccttcgggcaataagctctctgact	3000
Oy	3001	ataaagaaccccttgcaagctctcggtgtctctggbaaacactctccctgtgattctctgtgaaggg	3060
Dh	3001	ataaagaaccccttgcaagctctcggtgtctctggbaaacactctccctgtgattctctgtgaaggg	3060
Oy	3061	ggatgcttcgaaaggggaaaggagcgagagcctggaacagctggaacacaaaggggggtcgaaagg	3120
Dh	3061	ggatgcttcgaaaggggaaaggagcgagagcctggaacagctggaacacaaaggggggtcgaaagg	3120
Oy	3121	ggacagaaagcagcgaaagcctgggtctgctccatcgacttcctaacatgatacagtcgaagctc	3180
Dh	3121	ggacagaaagcagcgaaagcctgggtctgctccatcgacttcctaacatgatacagtcgaagctc	3180
Oy	3181	caggacggaaagccacaatgctctcagaaagaaagtccaatgaaaccaaagccacaatttctct	3240
Dh	3181	caggacggaaagccacaatgctctcagaaagaaagtccaatgaaaccaaagccacaatttctctct	3240
Oy	3241	tcctctaagcataagcacaatgagctatttgcacataacaaagaaatgacagagactaacgtgt	3300
Dh	3241	tcctctaagcataagcacaatgagctatttgcacataacaaagaaatgacagagactaacgtgtgt	3300
Oy	3301	ggtgagcttttgccggtgattccaaaagcttcggccagagcagctggaagaaatgccaagagattg	3360
Dh	3301	ggtgagcttttgccggtgattccaaaagcttcggccagagcagctggaagaaatgccaagagattg	3360
Oy	3361	ttaaactcttcaaccctgagccagagaccccaagcagctcagcagtgagctctgacagacagg	3420

[illegible]

[illegible]

PN WO95951779-A2.
PD 14-OCT-1999.
XX
XX
XX 07-APR-1999; 99WO-US07671.
PF 07-APR-1998; 98US-0056285.
XX
XX 07-APR-1998; 98US-0056285.
PR
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
XX Stone EM, Sheffield VC, Alward WLM, Fingert J;
PI WPI: 2000-022956/02.
XX
XX
XX Determination of a predisposition to glaucoma by analysing mutations in
PT the GLCIA gene -
XX
XX
XX Disclosure: Fig 1A; 137pp; English.
XX
XX The invention relates to a method for the determination of a
CC predisposition to glaucoma. The method comprises amplifying a GLCIA gen
CC with a primer pair selected from the sequences shown in 237981-238008.
CC The primers are used to determine whether a subject has or has the
CC potential to develop primary open wide angle glaucoma. The present
CC sequence represents the human GLCIA gene exon 1 and flanking sequences.
XX
XX Sequence 2800 BP; 781 A; 588 C; 673 G; 758 T; 0 other;

Query Match	Similarity	34.6%	Score 1836:	DB 21:	Length 2800:
Best Local	Similarity	99.5%:	Pred. No. 0:		
Matches 1864:	Conservative	0:	Mismatches	5:	Indels 5:
					Gaps 2:
QY	3431	agcgcaaggagagaaagaaagagagagatgtagttagagcaagaagacagattcat	3490		
Db	1	agcgcaaggagagagagaag-aaagagagagtagttagttagagcaagaagacagattcat	59		
QY	3491	tcaagggcagctgggaaatttaccacagggatctaatgccagtatcccttggtttcttagag	3550		
Db	60	tcaagggcagctgggaaatttaccacagggatctaatgccagtatcccttggtttcttagag	119		
QY	3551	gcagggctctattgtgggggggaaaaaatacagtctcaagggaagtcgggaacctgtattc	3610		
Db	120	gcagggctctattgtgggggggaaaaaatacagtctcaagggaagtcgggaacctgtattc	179		
QY	3611	aatactatactttccctctaccacagctgagtaattctctgagccaaagtcagtaactg	3670		
Db	180	aatactatactttccctctaccacagctgagtaattctctgagccaaagtcagtaactg	239		
QY	3671	aggcgctaaagtattacttggtttctcctctttagggaccttttctctctgtggagttagca	3730		
Db	240	aggcgctaaagtattacttgaattctcctctctttagggaccttttctctctgtggagttagca	299		
QY	3731	gcacaagagcaatcccggttctctttaaacygaagaacaacatctcctaagagtagtaagccaa	3790		
Db	300	gcacaagagcaatcccggttctctttaaacygaagaacaacatctcctaagagtagtaagccaa	359		
QY	3791	cagatccaagcctaaaggtctctgctgacatagtattggtttttagaaaaatcatcttcagcg	3850		
Db	360	cagatccaagcctaaaggtctctgctgacatagtattggtttttagaaaaatcatcttcagcg	419		
QY	3851	agctttaccatcttggttttcagaaaaagagagctgtagcccttggccaagctgtaaacaaca	3910		
Db	420	agctttaccatcttggttttcagaaaaagagagctgtagcccttggccaagctgtaaacaaca	479		
QY	3911	cccatctgttaaatgtctcagaagtcagagctctaaactgcagagacaatcaaatagaaataga	3970		
Db	480	cccatctgttaaatgtctcagaagtcagagctctaaactgcagagacaatcaaatagaaataga	539		
QY	3971	tcttttagagcaaacgtgttcttccaactctggaagtgagtcggccaaggaattggaaa	4030		
Db	540	tcttttagagcaaacgtgttcttccaactctggaagtgagtcggccaaggaattggaaa	599		

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OY 4031 taattcttcacagatctgacacgtctgtgtgtatataacacataaagtctgccaagg 4090
    |||
DB 600 taattcttcacagatctgacacgtctgtgtgtatataacacataaagtctgccaagg 659
OY 4091 caatcaatcttcagctgagctaaagtctctgacagcttctgtatattctgtgcta 4150
    |||
DB 660 caatcaatcttcagctgagctaaagtctctgacagcttctgtatattctgtgcta 719
OY 4151 tggccattctgctttctgtttctctctctgtgtgtattatataagcaaggattataa 4210
    |||
DB 720 tggccattctgctttctgtttctctctctgtgtgtattatataagcaaggattataa 779
OY 4211 cctacagctccagaagaagcctgtgaattgaaatgaggaataaatacgtttctattacc 4270
    |||
DB 780 cctacagctccagaagaagcctgtgaattgaaatgaggaataaatacgtttctattacc 839
OY 4271 acccttcaactaaatttaacatttattccattgagaaatagagccataaaccnaagtg 4330
    |||
DB 840 acccttcaactaaatttaacatttattccattgagaaatagagccataaaccnaagtg 899
OY 4331 taataagagtaacctgtgattgttcttaacaaatagaatacagagcattttactata 4390
    |||
DB 900 taataagagtaacctgtgattgttcttaacaaatagaatacagagcattttactata 959
OY 4391 ttaacagctgtgaggtacgtctgtaagtgaataatatactcaaaaactacttgaattc 4450
    |||
DB 960 ttaacagctgtgaggtacgtctgtaagtgaataatatactcaaaaactacttgaattc 1019
OY 4451 agaacctcctgctgagctctgttttaacataataaataaacaatgttaaaatttgat 4510
    |||
DB 1020 agaacctcctgctgagctctgttttaacataataaataaacaatgttaaaatttgat 1079
OY 4511 ttgtgaataatcatattcatattcatattgtttctctgtgttaactatattatattga 4570
    |||
DB 1080 ttgtgaataatcatattcatattcatattgtttctctgtgttaactatattatattga 1139
OY 4571 aaacacatctctctgagaagaagctcccaagattccacaaatagaagttctctgacatgaca 4630
    |||
DB 1140 aaacacatctctctgagaagaagctcccaagattccacaaatagaagttctctgacatgaca 1199
OY 4631 cacagagctaaagaatcttaagaagctaaacattgagctgtgacatgacaaagctg 4690
    |||
DB 1200 cacagagctaaagaatcttaagaagctaaacattgagctgtgacatgacaaagctg 1259
OY 4691 aaatttgaaagctctcccaagaatatacagaattgttttaagaagctagaagggtgagga 4750
    |||
DB 1260 aaatttgaaagctctcccaagaatatacagaattgttttaagaagctagaagggtgagga 1319
OY 4751 tctgacgctctctataagaatgctctccctgagacctgtgaggtgtgctgctgtgtct 4810
    |||
DB 1320 tctgacgctctctataagaatgctctccctgagacctgtgaggtgtgctgctgtgtct 1379
OY 4811 ggcctgacgttatttctctctgctccctgacagctcttaagaagctgttggatctccag 4870
    |||
DB 1380 ggcctgacgttatttctctctgctccctgacagctcttaagaagctgttggatctccag 1439
OY 4871 ttcctgacaaagctgagcagctgagcaagttctcaaatgagttctgacaaatgaaatgaaa 4930
    |||
DB 1440 ttcctgacaaagctgagcagctgagcaagttctcaaatgagttctgacaaatgaaatgaaa 1499
OY 4931 tataaagctagaataatactctgttgaatacagacacacagtagctccgtgtgaagtgtg 4990
    |||
DB 1500 tataaagctagaataatactctgttgaatacagacacacagtagctccgtgtgaagtgtg 1559
OY 4991 tgaacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5050
    |||
DB 1560 tgaacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1615
OY 5051 cttatttttgggtgataaggtgataaatttgagatgtttttttaaaagaactcccaaca 5110
    |||
DB 1616 cttatttttgggtgataaggtgataaatttgagatgtttttttaaaagaactcccaaca 1675
OY 5111 gactctgagaggttatttcttaagaatctctgtgacagctgaaagcaacccccctgtg 5170

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DB 1676 gactctgagaggttatttcttaagaatctctgtgacagctgaaagcaacccccctgtg 1735
    |||
OY 5171 cacagcccaacccagcctcaagctgctgacacctctgtcttccccaatgaaggctgctccc 5230
    |||
DB 1736 cacagcccaacccagcctcaagctgctgacacctctgtcttccccaatgaaggctgctccc 1795
OY 5231 cagtatataaaccctctcgtgagctcgggcatgagccagcaaggccacccatccaggcca 5290
    |||
DB 1796 cagtatataaaccctctcgtgagctcgggcatgagccagcaaggccacccatccaggcca 1855
OY 5291 cctctcagcagcagc 5304
    |||
DB 1856 cctctcagcagcagc 1869

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RESULT 10
O63862/c
ID O63862 standard; cDNA; 283 bp.
XX
AC O63862;
XX
DT 29-JAN-1995 (first entry)
XX
DE AP2 sequence obtd. by PCR for tumour specific DNA.
XX
KW Arbitrary primers; AP-PCR; amplification; tumour cells; cancer;
KW insertions; deletions; ss.
XX
OS Synthetic.
XX
PN WO9411531-A.
XX
PD 26-MAY-1994.
XX
PF 12-NOV-1993: 93WO-US10904.
XX
PR 13-NOV-1992: 92US-0975737.
XX
PA (CALB-) CALIFORNIA INST BIOLOGICAL RES.
PI Ionov Y, Malkhosyan S, McClelland M, Pelinado MA;
PI Perucho M, Welsh J;
XX
XX
DR MPI: 1994-183529/22.
XX
PT Identification of tumour cells - by analysing DNA to determine
PT whether insertions or deletions have occurred in reiterated
PT sequences
PS Disclosure: Page 52; 67pp: English.
XX
CC The sequence was obtd. by PCR with arbitrary PCR primers used to
CC detect insertions or deletions in DNA sequences. Such mutations are
CC markers of cancer so such primers can be used in the diagnosis of
CC cancer, esp. colorectal, stomach or pancreatic tumours.
CC See also Q63837-63.
XX
SQ Sequence 283 bp; 63 A; 77 C; 94 G; 49 T; 0 other:

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Query Match 3.3%; Score 176.4; DB 15; Length 283;
Best Local Similarity 80.4%; Pred. No. 2.9e-31;
Matches 222; Conservative 0; Mismatches 46; Indels 8; Gaps 1;

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OY 1281 gggctgaggtctgtgtcttaccctacatgctatgctctacacagctgacatgcaact 1340
    |||
DB 276 GAGTCTCGCTCTGCTGCGCCAGGCTGAGTGCACATGCGGCGCATCTCGGCTCATGCAACT 217
OY 1341 ctgcctcccaaggttcaagaatctctctgtctcagcctccgcgtgagctgagactcaagg 1400
    |||
DB 216 CCACCTCCCGGTTCAAGCATCTCTGCTCAGGCTCCCGAGTAGCTGGATTACAGG 157

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Oy	1401	CG-----cgcgcgcgcgaacttttgttatgtttgaagaagagggtttcacat	1452
Db	156	CGCGGCCACACCGCCCGGCTAATTTTGTATTTTGTAGAGAGCGGGTTTCACCATGT	97
Oy	1453	TAGccgcgcctgtgttccttgaactcctcgaacctcaagtgatcacaccacactcgcctcctaag	1512
Db	96	TGGCAGGCGCTGTGTCTTGAACCTCTGTGACCTCAGAGTGTATCCACCCACCTCGCCTCCCAAG	37
Oy	1513	tgtctggattacagcagatgacgtacacgcgcgcgcgcgc 1548	
Db	36	TGCTGGATTACAGGCTGTGAGCCACCGCCAGCC 1	
RESULT 11			
ID	286967/C		
XX	286967	standard; DNA: 162450 BP.	
AC	286967:		
XX	16-MAY-2000	(first entry)	
DT			
XX			
DE	Retinoblastoma binding protein-7 genomic DNA sequence.		
KW	RBP-7; retinoblastoma binding protein-7; abnormal cell proliferation;		
KW	diagnosis; therapy; cell differentiation; thyroid hyperplasia; psoriasis;		
KW	benign prostate hypertrophy; cancer; sarcoma; neoplasm; leukemia;		
KW	lymphoma; ds.		
XX			
OS	Homo sapiens.		
PN	WO200000607-A1.		
PD	06-JAN-2000.		
XX			
PF	30-JUN-1999; 99WO-IB01242.		
XX			
PR	30-JUN-1998; 98US-0091315.		
PR	10-DEC-1998; 98US-0111909.		
XX			
PA	(GEST) GENSET.		
XX			
PI	Bougueleret L.		
DR	WPI: 2000-117170/10.		
XX			
XX			
PT	Novel nucleic acid and polymorphic markers used for diagnosis of		
PT	diseases, especially those involving abnormal cell proliferation and		
PT	differentiation -		
PS			
PS	Claim 1; Page 118-163; 223pp; English.		
XX			
CC	This sequence represents the retinoblastoma binding protein-7 (RBP-7)		
CC	genomic sequence of the invention. The RBP-7 coding sequence and		
CC	regulatory sequences are useful for the recombinant production of the		
CC	protein and for expressing heterologous nucleic acids. Primers and probes		
CC	derived from the RBP-7 nucleotide sequence (e.g. 287035-287099) are		
CC	useful for DNA amplification and detection methods. RBP-7 biallelic		
CC	markers (see 286993-287034) are useful for diagnosis of disease related		
CC	to alteration in the regulation of in the coding regions of the RBP-7		
CC	gene and for prognosis/diagnosis of an eventual treatment with		
CC	therapeutic agents, especially agents acting on pathologies involving		
CC	abnormal cell proliferation and/or differentiation, these include		
CC	thyroid hyperplasia, psoriasis, benign prostate hypertrophy, cancers,		
CC	including breast cancer, sarcomas and other neoplasms, bladder cancer,		
CC	colon cancer, lung cancer, prostate cancer, various leukemias, and		
CC	lymphomas. RBP-7 antibodies are useful as diagnostic agents.		
XX			
XX	Sequence 162450 BP; 45465 A; 30661C; 32637 G; 53673 T; 14 other;		

OY	1280	aggatgaagagccttgcgttaacactccgtagtcctaacctcgaagcctcgaacc	1339
OY	1340	tctgctccccaaggtcaagaacaattctctgtctctaagcctcccgctagctggagtacaag	1399
DB	141865	TGCACCTCCCGGGTTCAAGGCAATTCTCCTGTCTGGCCTCCCAATAGCTGGACTACAG	141806
OY	1400	gcgcacgcccgacctaatlttttgtattgttagtagaagatggggtttcaccatatagcccg	1459
DB	141805	GCACACGCCCAAGCTAATTTTTGTATTTTTTAGCACAGATGGGGTTCACCCATTGTGTACG	141746
OY	1460	gctggtcttgaaacctccgaacctgaagtgatccaccaccaaccgaacctcctaaagtgcctgg	1519
DB	141745	GCTGGTCTCAAACCTCCTGACCCTCAGATGAITCCACTCCTCTCGGCTCTCCAAGTGCTGGG	141666
OY	1520	attaacagcatgaatcaccacgcccacgagc	1547
DB	141685	ATTACAGCTGTGAGCACACTGTGCCCCAGC	141658
RESULT	12		
ID	T62346/c		
XX	T62346	standard; DNA; 282 BP.	
AC	T62346:		
XX	DT	11-JUN-1997 (first entry)	
DE		Consensus Alu repeat sequence.	
XX		Bubble: interspersed repetitive element; ligation: annealing; primer:	
KW		PCG: polymerase chain reaction; amplification: chromosomal aberration;	
KW		genetic disorder: SS.	
KX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	primer_bind	22..45	
FT		/tag= a	
FT		/note= "binds primer 47-23 (T62347)"	
FT	primer_bind	216..236	
FT		/tag= b	
FT		/note= "binds either primer Alu-S (T62348) or	
FT		Alu-J (T62349)"	
FT	primer_bind	263..282	
FT		/tag= C	
FT		/note= "binds primer Alu-end (T62350)"	
XX			
PN	US5597694-A.		
PD	28-JAN-1997.		
XX			
PF	07-OCT-1993;	93US-0133629.	
XX			
PR	07-OCT-1993;	93US-0133629.	
XX			
PA	(MASI) MASSACHUSETTS INST TECHNOLOGY.		
PI	Housman DE, Munroe DJ;		
DR	WPI; 1997-108321/10.		
XX			
PT	Amplification of nucleic acid having interspersed repetitive element		
XX	- using bubble oligo:nucleotide		
PS	Disclosure: Column 19-20; 16pp; English.		
CC	The invention relates to the amplification of region of DNA containing		
CC	interspersed repetitive elements (IRE) such as the Alu repeat sequence		
CC	presented here. The method involves ligating a double stranded DNA		
CC	structure with a non-complementary region, a 'bubble', in the		

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XX

SQ Sequence 452 BP; 149 A; 92 C; 106 G; 85 T; 20 other;

Query Match	3.3%	Score 172.8	DB 17	Length 452
Best Local Similarity	86.4%	Pred. No. 2.3e-30		
Matches 204	Conservative	1	Mismatches 23	Indels 8
				Gaps 1

[illegible]

Search completed: December 3, 2000, 19:26:40
Job time: 43260 sec

